SEQUENCE LISTING

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- (i) APPLICANT:
 - (A) NAME: Akzo nobel n.v.
 - (B) STREET: Velperweg 76
 - (C) CITY: Arnhem
 - (E) COUNTRY: The Netherlands
 - (F) POSTAL CODE (ZIP): 6824 BM
 - (G) TELEPHONE: 0412-666379
 - (H) TELEFAX: 0412-650592
 - (I) TELEX: 37503 akpha nl

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- (ii) TITLE OF INVENTION: Novel estrogen receptor
- (iii) NUMBER OF SEQUENCES: 28
- 20
- (iv) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

د په۔

- (2) INFORMATION FOR SEQ ID NO: 1:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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- (ii) MOLECULE TYPE: cDNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC 60 ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC 120 CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA 180 GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC 240 GCCAGCCCTG TTACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC 300 GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT 360 AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420 GATAAAAACC GGCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480 ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA 540 AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC 600 CGAGTGCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG 660 720 GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC ATGATGATGT CCCTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC 780 AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTCGACC AAGTGCGGCT CTTGGAGAGC 840 TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCCGGCAAG 900 CTCATCTTTG CTCCAGATCT TGTTCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT 960 CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA 1020 CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG 1080 GTCACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG 1140

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ACCGATGCTT TGGTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200

CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGTAA CAAGGGCATG 1260

GAACATCTGC TCAACATGAA GTGCAAAAAT GTGGTCCCAG TGTATGACCT GCTGCTGGAG 1320

ATGCTGAATG CCCACGTGCT TCGCGGGTGC AAGTCCTCCA TCACGGGGTC CGAGTGCAGC 1380

CCGGCAGAGG ACAGTAAAAG CAAAGAGGGC TCCCAGAACC CACAGTCTCA GTGA 1434

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1251 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC 60 ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC 120 CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA 180 GAACACCCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC 240 GCCAGCCCTG TTACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC 300 GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT 360 AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC 420 GATAAAAACC GGCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA 480

ATGGTGAAGT	GTGGCTCCCG	GAGAGAGAGA	TGTGGGTACC	GCCTTGTGCG	GAGACAGAGA	540
AGTGCCGACG	AGCAGCTGCA	CTGTGCCGGC	AAGGCCAAGA	GAAGTGGCGG	CCACGCGCCC	600
CGAGTGCGGG	AGCTGCTGCT	GGACGCCCTG	AGCCCCGAGC	AGCTAGTGCT	CACCCTCCTG	660
GAGGCTGAGC	CGCCCCATGT	GCTGATCAGC	CGCCCCAGTG	CGCCCTTCAC	CGAGGCCTCC	720
ATGATGATGT	CCCTGACCAA	GTTGGCCGAC	AAGGAGTTGG	TACACATGAT	CAGCTGGGCC	780
AAGAAGATTC	CCGGCTTTGT	GGAGCTCAGC	CTGTTCGACC	AAGTGCGGCT	CTTGGAGAGC	840
TGTTGGATGG	AGGTGTTAAT	GATGGGGCTG	ATGTGGCGCT	CAATTGACCA	CCCCGGCAAG	900
CTCATCTTTG	CTCCAGATCT	TGTTCTGGAC	AGGGATGAGG	GGAAATGCGT	AGAAGGAATT	960
CTGGAAATCT	TTGACATGCT	CCTGGCAACT	ACTTCAAGGT	TTCGAGAGTT	AAAACTCCAA	1020
CACAAAGAAT	ATCTCTGTGT	CAAGGCCATG	ATCCTGCTCA	ATTCCAGTAT	GTACCCTCTG	1080
GTCACAGCGA	CCCAGGATGC	TGACAGCAGC	CGGAAGCTGG	CTCACTTGCT	GAACGCCGTG	1140
ACCGATGCTT	TGGTTTGGGT	GATTGCCAAG	AGCGGCATCT	CCTCCCAGCA	GCAATCCATG	1200
CGCCTGGCTA	ACCTCCTGAT	GCTCCTGTCC	CACGTCAGGC	ATGCGAGGTG	A	1251

(2) INFORMATION FOR SEQ ID NO: 3:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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5	Cy:	s Ala	Val	Cys	Ser 5	Asp	Туr	Ala	Ser	Gly 10	Tyr	His	Tyr	Gly	Val 15	Trp
,	Se	c Cys	Glu	Gly 20	Cys	Lys	Ala	Phe	Phe 25	Lys	Arg	Ser	Ile	Gln 30	Gly	His
10	Ası	n Asp	Tyr 35	Ile	Cys	Pro	Ala	Thr 40	Asn	Gln	Cys	Thr	Ile 45	Asp	Lys	Asn
	Arç	g Arg 50	Lys	Ser	Cys	Gln	Ala 55	Cys	Arg	Leu	Arg	Lys 60	Cys	Tyr	Glu	Val
15	Gl ₃ 65	/ Met														
	(2) INFO	ORMAT:	ON E	OR S	EQ I	D NC	: 4:									
20	(i)	(B (C) LEN) TYI) STI	E CHA NGTH: PE: a RANDA	233 mino EDNES	3 ami o aci 55: s	ino a id singl	cids	3							
.25	(ii) MOL	ECUL	Е ТҮІ	PE: p	pepti	ide									
30	(xi) SEQ	UENC	E DE:	SCRI	PTIO	N: S	EQ I	D NO	: 4:						
	Le 1	u Val	Leu	Thr	Leu 5	Leu	Glu	Ala	Glu	Pro 10	Pro	His	Val	Leu	Ile 15	Ser
35	Ar	g Pro	Ser	Ala 20	Pro	Phe	Thr	Glu	Ala 25	Ser	Met	Met	Met	Ser 30	Leu	Thr
	Ly	s Leu	Ala 35	Asp	Lys	Glu	Leu	Val 40	His	Met	Ile	Ser	Trp 45	Ala	Lys	Lys

	Ile	Pro 50	Gly	Phe	Val	Glu	Leu 55	Ser	Leu	Phe	Asp	Gln 60	Val	Arg	Leu	Leu
5	Glu 65	Ser	Cys	Trp	Met	Glu 70	Val	Leu	Met	Met	Gly 75	Leu	Met	Trp	Arg	Ser 80
10	Ile	Asp	His	Pro	Gly 85	Lys	Leu	Ile	Phe	Ala 90	Pro	Asp	Leu	Val	Leu 95	Asp
	Arg	Asp	Glu	Gly 100	Lys	Cys	Val	Glu	Gly 105	Ile	Leu	Glu	Ile	Phe 110	Asp	Met
15	Leu	Leu	Ala 115	Thr	Thr	Ser	Arg	Phe 120	Arg	Glu	Leu	Lys	Leu 125	Gln	His	Lys
	Glu	Туг 130	Leu	Cys	Val	Lys	A la 135	Met	Ile	Leu	Leu	Asn 140	Ser	Ser	Met	Tyr
20	Pro 145	Leu	Val	Thr	Ala	Thr 150	Gln	Asp	Ala	Asp	Ser 155	Ser	Arg	Lys	Leu	Ala 160
	145				Ala Ala 165	150					155					160
25	145 His	Leu	Leu	Asn	Ala	150 Val	Thr	Asp	Ala	Leu 170	155 Val	Trp	Val	Ile	Ala 175	160 Lys
	145 His	Leu Gly	L e u	Asn Ser 180	Ala 165	150 Val Gln	Thr	Asp Gln His	Ala Ser 185	Leu 170 Met	155 Val Arg	Trp Leu	Val Ala	Ile Asn 190 Met	Ala 175 Leu	160 Lys Leu
25	145 His Ser Met	Leu Gly Leu	Leu Ile Leu 195 Asn	Asn Ser 180 Ser	Ala 165 Ser His	Val Gln Val	Thr Gln Arg	Asp Gln His 200 Asn	Ala Ser 185 Ala	Leu 170 Met	155 Val Arg Asn	Trp Leu Lys	Val Ala Gly 205 Tyr	Ile Asn 190 Met	Ala 175 Leu Glu	160 Lys Leu

(i) SEQUENCE CHARACTERISTICS:

		(A)	LEN	IGTH:	477	ami	ino a	cids	5								
		(B)	TYE	PE: a	mino	aci	ld										
		(C)	STF	RANDE	DNES	SS: 5	singl	.е									
5		(D)	TOE	oroc	γ: υ	ınkno	own										
	(ii)	MOLE	ECULE	E TYP	E: F	rote	ein										
10																	
	(xi)	SEQU	JENCE	E DES	CRIE	OITS	l: SE	EQ II	NO:	5:							
O																	
	Met	Asn	Tyr	Ser	Ile	Pro	Ser	Asn	Val		Asn	Leu	Glu	Gly		Pro	
	1				5					10					15		
15															_		
	Gly	Arg	Gln		Thr	Ser	Pro	Asn	Val	Leu	Trp	Pro	Thr		Gly	His	
				20					25					30			
	_	_	_	_			***		G1	7	C	TT: -	T	m	N1 -	C1	
	Leu	Ser		Leu	Val	Val	HIS		Gln	Leu	ser	піз	15 45	ıyı	ALA	GIU	
20			35					40					43				
	Dwa	C1-	T	°0-	Dro	Trn	Cue	Glu	Ala	Ara	Ser	T.e.ii	Glu	Hig	Th r	T.e.u	
	PIO	50	пуз	ser	110	пр	55	GIU	7114	7119	501	60	014			200	
		30					33										
25	Pro	Val	Asn	Ara	Glu	Thr	Leu	Lvs	Arg	Lys	Val	Ser	Gly	Asn	Arg	Cys	
	65					70		-	_	-	75		_			80	
	Ala	Ser	Pro	Val	Thr	Gly	Pro	Gly	Ser	Lys	Arg	Asp	Ala	His	Phe	Cys	
					85					90					95		
30																	
	Ala	Val	Cys	Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser	
				100					105					110			
	Cys	Glu	Gly	Cys	Lys	Ala	Phe	Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn	•
35			115					120					125				
	Asp	Tyr	Ile	Cys	Pro	Ala	Thr	Asn	Gln	Cys	Thr			Lys	Asn	Arg	
		130)				135					140					

	145	гÀг	ser	Cys	GIU	150	Cys	Arg	Leu	Arg	155	Суз	TYL	Giu	Val	160	
5	Met	Val	Lys	Cys	Gly 165	Ser	Arg	Arg	Glu	A rg 170	Cys	Gly	Tyr	Arg	Leu 175	Val	
	Arg	Arg	Gln	Arg 180	Ser	Ala	Asp	Glu	Gln 185	Leu	His	Cys	Ala	Gly 190	Lys	Ala	
10	Lys	Arg	Ser 195	Gly	Gly	His	Ala	Pro 200	Arg	Val	Arg	Glu	Leu 205	Leu	Leu	Asp	
اً. 15	Ala	Leu 210	Ser	Pro	Glu	Gln	Leu 215	Val	Leu	Thr	Leu	Leu 220	Glu	Ala	Glu	Pro	
13	Pro 225	His	Val	Leu	Ile	Ser 230	Arg	Pro	Ser	Ala	Pro 235	Phe	Thr	Glu		Ser 240	
20	Met	Met	Met	Ser	Leu 2 4 5	Thr	Lys	Leu	Ala	As p 250	Lys	Glu	Leu	Val	His 255	Met	
	Ile	Ser	Trp	Ala 260	Lys	Lys	Ile	Pro	Gly 265	Phe	Val	Glu	Leu	Ser 270	Leu	Phe	
25	Asp	Gln	Val 275	Arg	Leu	Leu	Glu	Ser 280	Cys	Trp	Met	Glu	Val 285	Leu	Met	Met	
30	Gly	Leu 290	Met	Trp	Arg	Ser	Ile 295	Asp	His	Pro	Gly	Lys 300	Leu	Ile	Phe	Ala	
	Pro 305	_	Leu	Val	Leu	Asp 310	Arg	Asp	Glu	Gly	Lys 315	Cys	Val	Glu	Gly	Ile 320	
35	Leu	Glu	Ile	Phe	Asp 325		Leu	Leu	Ala	Thr 330		Ser	Arg	Phe	Arg 335	Glu	,
	Leu	Lys	Leu	Gln 340		Lys	Glu	Tyr	Leu 345		Val	Lys	Ala	Met 350		Leu	

	Leı	ı Asn	Ser 355	Ser	Met	Tyr	Pro	Leu 360	Val	Thr	Ala	Thr	Gln 365	Asp	Ala	Asp
5	Sei	s Ser 370	Arg	Lys	Leu	Ala	His 375	Leu	Leu	Asn	Ala	Val 380	Thr	Asp	Ala	Leu
	Va] 385	Trp	Val	Ile	Ala	Lys 390	Ser	Gly	Ile	Ser	Ser 395	Gln	Gln	Gln	Ser	Met 400
10	Arç	, Leu	Ala	Asn	Leu 405	Leu	Met	Leu	Leu	Ser 410	His	Val	Arg	His	Ala 415	Ser
)	Asr	Lys	Gly	Met 420	Glu	His	Leu	Leu	Asn 425	Met	Lys	Cys	Lys	Asn 430	Val	Val
15	Pro	Val	Tyr 435	Asp	Leu	Leu	Leu	Glu 440	Met	Leu	Asn	Ala	His 445	Val	Leu	Arg
20	Gly	Cys 450	Lys	Ser	Ser	Ile	Thr 455	Gly	Ser	Glu	Cys	Ser 460	Pro	Ala	Glu	Asp
	Se:	Lys	Ser	Lys	Glu	Gly 470	Ser	Gln	Asn	Pro	Gln 475	Ser	Gln			
25	(2) INFO	RMAT	ION 1	FOR :	SEQ :	ID N	o: 6	:								
	(i)	•) LE	NGTH	: 41	6 am	ino (s							
30		(C) TY) ST) TO	RAND	EDNE	ss:	sing	le								
	(ii) MOL	ECUL	Е ТҮ	PE:	prot	ein									
2.5																

Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn Leu Glu Gly Gly Pro

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

	1				5					10					15	
_	Gly	Arg	Gln	Thr 20	Thr	Ser	Pro	Asn	Val 25	Leu	Trp	Pro	Thr	Pro 30	Gly	His
5	Leu	Ser	Pro 35	Leu	Val	Val	His	Arg 40	Gln	Leu	Ser	His	Leu 45	Tyr	Ala	Glu
10	Pro	Gln 50	Lys	Ser	Pro	Trp	Cys 55	Glu	Ala	Arg		Leu 60	Glu	His	Thr	Leu
	Pro 65	Val	Asn	Arg	Glu	Thr 70	Leu	Lys	Arg	Lys	Val 75	Ser	Gly	Asn		Cys 80
15	Ala	Ser	Pro	Val	Thr 85	Gly	Pro	Gly	Ser	Lys 90	Arg	Asp	Ala		Phe 95	Cys
	Ala	Val	Cys	Ser 100	Asp	Tyr	Ala	Ser	Gly 105	Tyr	His	Tyr	Gly	Val 110	Trp	Ser
20	Cys	Glu	Gly 115	Суѕ	Lys	Ala	Phe	Phe 120	Lys	Arg	Ser	Ile	Gln 125	Gly	His	Asn
25	Asp	Туг 130	Ile	Суз	Pro	Ala	Thr 135	Asn	Gln	Cys	Thr	Ile 140	Asp	Lys	Asn	Arg
• "	Arg 145	Lys	Ser	Cys	Gln	Ala 150	Cys	Arg	Leu	Arg	Lys 155	Cys	Tyr	Glu	Val	Gly 160
30	Met	Val	Lys	Cys	Gly 165	Ser	Arg	Arg	Glu	Arg 170	Cys	Gly	Tyr	Arg	Leu 175	Val
	Arg	Arg	Gln	A rg		Ala	Asp	Glu	Gln 185		His	Cys	Ala	Gly 190		Ala
35	Lys	Arg	9 Ser 195		Gly	His	Ala	Pro		Val	Arg	Glu	Leu 205		Leu	Asp
			193	,												

		210					215					220				
_	Pro 225	His	Val	Leu		Ser . 230	Arg	Pro	Ser	Ala	Pro 235	Phe	Thr	Glu	Ala	Ser 240
5	Met	Met	Met		Leu 2 4 5	Thr	Lys	Leu	Ala	As p 250	Lys	Glu	Leu	Val	His 255	Met
10	Ile	Ser	Trp	Ala 260	Lys	Lys	Ile	Pro	Gl y 265	Phe	Val	Glu	Leu	Ser 270	Leu	Phe
	Asp	Gln	Val 275	Arg	Leu	Leu	Glu	Ser 280	Cys	Trp	Met		Val 285	Leu	Met	Met
15	Gly	Leu 290	Met	Trp	Arg		Ile 295	Asp	His	Pro	Gly	Lys 300	Leu	Ile	Phe	Ala
20	Pro 305	Asp	Leu	Val	Leu	Asp 310	Arg	Asp	Glu	Gly	Lys 315	Cys	Val	Glu	Gly	11e 320
20	Leu	Glu	Ile	Phe	Asp 325	Met	Leu	Leu	Ala	Thr 330	Thr	Ser	Arg	Phe	Arg 335	Glu
25	Leu	Lys	Leu	Gln 340	His	Lys	Glu	Tyr	Leu 345	Суз	Val	Lys	Ala	Met 350	Ile	Leu
	Leu	Asn	Ser 355		Met	Tyr	Pro	Leu 360	Val	Thr	Ala	Thr	Gln 365	Asp	Ala	Asp
30	Ser	Ser 370		Lys	Leu	Ala	His 375		Leu	Asn	Ala	Val 380		Asp	Ala	Leu
35	Val 385		Val	. Ile	Ala	Lys 390		Gly	' Ile	: Ser	Ser 395		Gln	Gln	Ser	Met 400
	Arg	Lev	ı Ala	a Asn	105		Met	: Lev	ı Lev	1 Ser 410		. Val	Arg	g His	Ala 415	Arg

	(2) INFORMATION FOR SEQ ID NO: 7:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 29 base pairs	
5	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: both	
	(D) TOPOLOGY: unknown	
10	(ii) MOLECULE TYPE: cDNA	
> .		
ø ^g	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:	
15	GGIGAYGARG CWTCIGGITG YCAYTAYGG	29
	(2) INFORMATION FOR SEQ ID NO: 8:	
	(i) SEQUENCE CHARACTERISTICS:	
20	(A) LENGTH: 29 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:	
30	AAGCCTGGSA YICKYTTIGC CCAIYTIAT	29
	(2) INFORMATION FOR SEQ ID NO: 9:	
		•
35	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 22 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	

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	(ii) MOLECULE TYPE: cDNA	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:	
	TGTTACGAAG TGGGAATGGT GA	22
10	(2) INFORMATION FOR SEQ ID NO: 10:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid	
15	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
20		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:	
25	TTGACACCAG ACCAACTGGT AATG	24
-	(2) INFORMATION FOR SEQ ID NO: 11:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs	
20	(B) TYPE: nucleic acid	
30	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
2.5	(ii) MOLECULE TYPE: cDNA	•
35		

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

	GGTGGCGACG ACTCCTGGAG CCCG	24
	(2) INFORMATION FOR SEQ ID NO: 12:	
5	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 22 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: cDNA	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:	
	GTACACTGAT TTGTAGCTGG AC	22
	(2) INFORMATION FOR SEQ ID NO: 13:	
20	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
25	(D) TOPOLOGY: linear	
•	(ii) MOLECULE TYPE: cDNA	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:	
	CCATGATGAT GTCCCTGACC	20
35	(2) INFORMATION FOR SEQ ID NO: 14:	•
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs	
	(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single

	(D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: cDNA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:	
10	TCGCATGCCT GACGTGGGAC	20
a.	(2) INFORMATION FOR SEQ ID NO: 15:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: cDNA	
· २ ,5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:	24
	(2) INFORMATION FOR SEQ ID NO: 16:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	•
35	(::) MOLECULE TYPE: CDMA	
	(ii) MOLECULE TYPE: cDNA	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:	
	GGAAGCTGGC TCACTTGCTG	20
5	(2) INFORMATION FOR SEQ ID NO: 17:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs	
	(B) TYPE: nucleic acid	
10	(C) STRANDEDNESS: single	
<u> </u>	(D) TOPOLOGY: linear	
فن	(ii) MOLECULE TYPE: cDNA	
15		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:	
20	TCTTGTTCTG GACAGGGATG	20
20	(2) INFORMATION FOR SEQ ID NO: 18:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 20 base pairs	
25	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
30		
	(W.) CHOURNER DESCRIPTION, SEC. ID NO. 19.	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:	•
35	GCATGGAACA TCTGCTCAAC	20
	(2) INFORMATION FOR SEQ ID NO: 19:	

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 21 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
5		
	(ii) MOLECULE TYPE: cDNA	
1.0	(will appropriate the second	
10	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:	
	AGCAAGTTCA GCCTGTTAAG T	21
	AGGARGITER GOOTGITANG I	21
	(2) INFORMATION FOR SEQ ID NO: 20:	
15		
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 1257 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: double	
20	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
25		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:	
	(MI) DEGORMED DESCRIPTION. SEQ ID NO. 20.	
	ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC	60
30	ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC	120
	CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA	180
		•
	GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC	,24 0
35		
	GCCAGCCCTG TTACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC	300
	GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT	360
	GATTACGCAT COGGATATCA CTATGGAGTC TOGTCGTGTG AAGGATGTAA GGCCTTTTT	360

AAAAGAAGCA	TTCAAGGACA	TAATGATTAT	ATTTGTCCAG	CTACAAATCA	GTGTACAATC	420
GATAAAAACC	GGCGCAAGAG	CTGCCAGGCC	TGCCGACTTC	GGAAGTGTTA	CGAAGTGGGA	480
ATGGTGAAGT	GTGGCTCCCG	GAGAGAGAGA	TGTGGGTACC	GCCTTGTGCG	GAGACAGAGA	540
AGTGCCGACG	AGCAGCTGCA	CTGTGCCGGC	AAGGCCAAGA	GAAGTGGCGG	CCACGCGCCC	600
CGAGTGCGGG	AGCTGCTGCT	GGACGCCCTG	AGCCCCGAGC	AGCTAGTGCT	CACCCTCCTG	660
GAGGCTGAGC	CGCCCCATGT	GCTGATCAGC	CGCCCCAGTG	CGCCCTTCAC	CGAGGCCTCC	720
ATGATGATGT	CCCTGACCAA	GTTGGCCGAC	AAGGAGTTGG	TACACATGAT	CAGCTGGGCC	780
AAGAAGATTC	CCGGCTTTGT	GGAGCTCAGC	CTGTTCGACC	AAGTGCGGCT	CTTGGAGAGC	840
TGTTGGATGG	AGGTGTTAAT	GATGGGGCTG	ATGTGGCGCT	CAATTGACCA	CCCCGGCAAG	900
CTCATCTTTG	CTCCAGATCT	TGTTCTGGAC	AGGGATGAGG	GGAAATGCGT	AGAAGGAATT	960
CTGGAAATCT	TTGACATGCT	CCTGGCAACT	ACTTCAAGGT	TTCGAGAGTT	AAAACTCCAA	1020
CACAAAGAAT	ATCTCTGTGT	CAAGGCCATG	ATCCTGCTCA	ATTCCAGTAT	GTACCCTCTG	1080
GTCACAGCGA	CCCAGGATGC	TGACAGCAGC	CGGAAGCTGG	CTCACTTGCT	GAACGCCGTG	1140
ACCGATGCTT	TGGTTTGGGT	GATTGCCAAG	AGCGGCATCT	CCTCCCAGCA	GCAATCCATG	1200
CGCCTGGCTA	ACCTCCTGAT	GCTCCTGTCC	CACGTCAGGC	ATGCGAGGTC	TGCCTGA	1257

(2) INFORMATION FOR SEQ ID NO: 21:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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	(xi)	SEQ	JENCI	E DES	SCRI	PTIO	V: SI	EQ II	ONO:	21:	:					
5	Met 1	Asn	Tyr	Ser	Ile 5	Pro	Ser	Asn	Val	Thr 10	Asn	Leu	Glu	Gly	Gly 15	Pro
10	Gly	Arg	Gln	Thr 20	Thr	Ser	Pro	Asn	Val 25	Leu	Trp	Pro	Thr	Pro 30	Gly	His
0	Leu	Ser	Pro 35	Leu	Val	Val	His	Arg 40	Gln	Leu	Ser	His	Leu 45	Tyr	Ala	Glu
15	Pro	Gln 50	Lys	Ser	Pro	Trp	Cys 55	Glu	Ala	Arg	Ser	Leu 60	Glu	His	Thr	Leu
20	Pro 65	Val	Asn	Arg	Glu	Thr 70	Leu	Lys	Arg	Lys	Val 75	Ser	Gly	Asn	Arg	С уз 80
	Ala	Ser	Pro	Val	Thr 85	Gly	Pro	Gly	Ser	Lys 90	Arg	Asp	Ala	His	Phe 95	Сув
25	Ala	Val	Суѕ	Ser 100	Asp	Tyr	Ala	Ser	Gly 105	Туr	His	Tyr	Gly	Val 110	Trp	Ser
	Cys	Glu	Gly 115	Cys	Lys	Ala	Phe	Phe 120	Lys	Arg	Ser	Ile	Gln 125	Gly	His	Asn
30	Asp	Туг 130	Ile	Cys	Pro	Ala	Thr 135	Asn	Gln	Cys	Thr	Ile 140	Asp	Lys	Asn	Arg
35	Arg 145	Lys	Ser	Cys	Gln	Ala 150	Cys	Arg	Leu	Arg	Lys 155	Cys	Tyr	Glu	Val	Gly 160
	Met	Val	Lys	Cys	Gly 165		Arg	Arg	Glu	A rg 170		Gly	Tyr	Arg	Leu 175	Val
	Ara	Ara	Gln	Ara	Ser	Ala	Asn	Glu	Gln	Leu	His	Cvs	Ala	Glv	Lvs	Ala

Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala Val Thr Asp Ala Leu

Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser Gln Gln Gln Ser Met

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385

Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His Val Arg His Ala Arg 405 410 5 Ser Ala (2) INFORMATION FOR SEQ ID NO: 22: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 34 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 15 (ii) MOLECULE TYPE: cDNA 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22: 34 CTTGGATCCA TAGCCCTGCT GTGATGAATT ACAG (2) INFORMATION FOR SEQ ID NO: 23: _ 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single 30 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GATGGATCCT CACCTCAGGG CCAGGCGTCA CTG

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1898 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CACGAATCTT TGAGAACATT ATAATGACCT TTGTGCCTCT TCTTGCAAGG TGTTTTCTCA 60 GCTGTTATCT CAAGACATGG ATATAAAAAA CTCACCATCT AGCCTTAATT CTCCTTCCTC 120 CTACAACTGC AGTCAATCCA TCTTACCCCT GGAGCACGGC TCCATATACA TACCTTCCTC 180 CTATGTAGAC AGCCACCATG AATATCCAGC CATGACATTC TATAGCCCTG CTGTGATGAA 240 TTACAGCATT CCCAGCAATG TCACTAACTT GGAAGGTGGG CCTGGTCGGC AGACCACAAG 300 CCCAAATGTG TTGTGGCCAA CACCTGGGCA CCTTTCTCCT TTAGTGGTCC ATCGCCAGTT 360 ATCACATCTG TATGCGGAAC CTCAAAAGAG TCCCTGGTGT GAAGCAAGAT CGCTAGAACA 420 CACCTTACCT GTAAACAGAG AGACACTGAA AAGGAAGGTT AGTGGGAACC GTTGCGCCAG 480 CCCTGTTACT GGTCCAGGTT CAAAGAGGGA TGCTCACTTC TGCGCTGTCT GCAGCGATTA 540 CGCATCGGGA TATCACTATG GAGTCTGGTC GTGTGAAGGA TGTAAGGCCT TTTTTAAAAG 600 AAGCATTCAA GGACATAATG ATTATATTTG TCCAGCTACA AATCAGTGTA CAATCGATAA 660 AAACCGGCGC AAGAGCTGCC AGGCCTGCCG ACTTCGGAAG TGTTACGAAG TGGGAATGGT 720

GAAGTGTGGC TCCCGGAGAG AGAGATGTGG GTACCGCCTT GTGCGGAGAC AGAGAAGTGC 780 CGACGAGCAG CTGCACTGTG CCGGCAAGGC CAAGAGAAGT GGCGGCCACG CGCCCCGAGT 840 GCGGGAGCTG CTGCTGGACG CCCTGAGCCC CGAGCAGCTA GTGCTCACCC TCCTGGAGGC 900 TGAGCCGCCC CATGTGCTGA TCAGCCGCCC CAGTGCGCCC TTCACCGAGG CCTCCATGAT 960 GATGTCCCTG ACCAAGTTGG CCGACAAGGA GTTGGTACAC ATGATCAGCT GGGCCAAGAA 1020 GATTCCCGGC TTTGTGGAGC TCAGCCTGTT CGACCAAGTG CGGCTCTTGG AGAGCTGTTG 1080 GATGGAGGTG TTAATGATGG GGCTGATGTG GCGCTCAATT GACCACCCCG GCAAGCTCAT 1140 CTTTGCTCCA GATCTTGTTC TGGACAGGGA TGAGGGGAAA TGCGTAGAAG GAATTCTGGA 1200 AATCTTTGAC ATGCTCCTGG CAACTACTTC AAGGTTTCGA GAGTTAAAAC TCCAACACAA 1260 AGAATATCTC TGTGTCAAGG CCATGATCCT GCTCAATTCC AGTATGTACC CTCTGGTCAC 1320 AGCGACCCAG GATGCTGACA GCAGCCGGAA GCTGGCTCAC TTGCTGAACG CCGTGACCGA 1380 TGCTTTGGTT TGGGTGATTG CCAAGAGCGG CATCTCCTCC CAGCAGCAAT CCATGCGCCT 1440 1500 GGCTAACCTC CTGATGCTCC TGTCCCACGT CAGGCATGCG AGTAACAAGG GCATGGAACA TCTGCTCAAC ATGAAGTGCA AAAATGTGGT CCCAGTGTAT GACCTGCTGC TGGAGATGCT 1560 GAATGCCCAC GTGCTTCGCG GGTGCAAGTC CTCCATCACG GGGTCCGAGT GCAGCCCGGC 1620 AGAGGACAGT AAAAGCAAAG AGGGCTCCCA GAACCCACAG TCTCAGTGAC GCCTGGCCCT 1680 GAGGTGAACT GGCCCACAGA GGTCACAAGC TGAAGCGTGA ACTCCAGTGT GTCAGGAGCC 1740 TGGGCTTCAT CTTTCTGCTG TGTGGTCCCT CATTTGGTGA TGGCAGGCTT GGTCATGTAC 1800 CATCCTTCCC TCCACCTTCC CAACTCTCAG GAGTCGGTGT GAGGAAGCCA TAGTTTCCCT 1860

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	TGTTAGCA	GA GG	GACA	TTTG	TAA	'CG A G	CGT	TTCC	ACAC	:							1898
	(2) INFO	RMATI	ON E	FOR S	EQ I	D NC): 25	:									
5	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 530 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 																
10	(ii)	MOLE	CULF	C TYP	E: p	epti	de										
	(11)				-· F	-F											
15	(x i)	SEQU	JENCE	E DES	CRIP	TION	: SE	Q IE	NO:	25:							
20	Met 1	Asp	Ile	Lys	As n 5	Ser	Pro	Ser	Ser	Leu 10	Asn	Ser	Pro	Ser	Ser 15	Tyr	
20	Asn	Cys	Ser	Gln 20	Ser	Ile	Leu	Pro	Leu 25	Glu	His	Gly	Ser	Ile 30	Tyr	Ile	
25	Pro	Ser	Ser 35	Tyr	Val	Asp	Ser	His 40	His	Glu	Tyr	Pro	Ala 45	Met	Thr	Phe	
•	Туг	Ser 50	Pro	Ala	Val	Met	As n 55	Tyr	Ser	Ile	Pro	Ser 60	Asn	Val	Thr	Asn	
30	Le u 65	Glu	Gly	Gly	Pro	Gly 70	Arg	Gln	Thr	Thr	Ser 75	Pro	Asn	Val	Leu	Trp 80	
	Pro	Thr	Pro	Gly	His 85	Leu	Ser	Pro	Leu	Val 90	Val	His	Arg	Gln	Leu 95	Ser	•

His Leu Tyr Ala Glu Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser 105

Leu Glu His Thr Leu Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val

100

110

5	Ser	Gly 130	Asn	Arg	Cys	Ala	Ser 135	Pro	Val	Thr	Gly	Pro 140	Gly	Ser	Lys	Arg
ý ,	Asp 145	Ala	His	Phe	Cys	Ala 150	Val	Cys	Ser	Asp	Туг 155	Ala	Ser	Gly	Tyr	His 160
10	Tyr	Gly	Val	Trp	Ser 165	Cys	Glu	Gly	Cys	Lys 170	Ala	Phe	Phe	Lys	Arg 175	Ser
•	Ile	Gln	Gly	His 180	Asn	Asp	Tyr	Ile	Cys 185	Pro	Ala	Thr	Asn	Gln 190	Cys	Thr
15	Ile	Asp	Lys 195	Asn	Arg	Arg	Lys	Ser 200	Cys	Gln	Ala	Cys	Arg 205	Leu	Arg	Lys
	Cys	Туг 210	Glu	Val	Gly	Met	Val 215	Lys	Cys	Gly	Ser	Arg 220	Arg	Glu	Arg	Cys
20	Gly 225	Tyr	Arg	Leu	Val	A rg 230	Arg	Gln	Arg	Ser	Ala 235	Ąsp	Glu	Gln	Leu	His 240
_25	Cys	Ala	Gly	Lys	Ala 245	Lys	Arg	Ser	Gly	Gly 250	His	Ala	Pro	Arg	Val 255	Arg
	Glu	Leu	Leu	Leu 260	Asp	Ala	Leu	Ser	Pro 265	Glu	Gln	Leu	Val	Leu 270	Thr	Leu
30	Leu	Glu	Ala 275		Pro	Pro	His	Val 280	Leu	Ile	Ser	Arg	Pro 285		Ala	Pro
	Phe	Thr 290		Ala	Ser	Met	M et 295		Ser	Leu	Thr	Lys 300		Ala	Asp	Lys
35	Glu 305		ı Val	His	. Met	310		Trp	Ala	Lys	Lys		Pro	Gly	Phe	Val 320

					325					330					335	
	Glu	Val	Leu	Met 340	Met	Gly	Leu	Met	Trp 345	Arg	Ser	Ile	Asp	His 350	Pro	Gly
5	Lys	Leu	Ile 355	Phe	Ala	Pro	Asp	Leu 360	Val	Leu	Asp	Arg	Asp 365	Glu	Gly	Lys
	Cys	Val		Gly	Ile	Leu			Phe	Asp	Met			Ala	Thr	Thr
10	Ser	370 Arg	Phe	Ara	Glu	Leu	375 Lvs	Leu	Gln	His	Lvs	380 Glu	Tvr	Leu	Cvs	Val
6)	385					390	-1-				395		-1-		-4-	400
15	Lys	Ala	Met	Ile	Leu 405	Leu	Asn	Ser	Ser	Met 410	Tyr	Pro	Leu	Val	Thr 415	Ala
	Thr	Gln	Asp	Ala 420	Asp	Ser	Ser	Arg	Lys 425	Leu	Ala	His	Leu	Leu 430	Asn	Ala
20	Val	Thr	Asp 435	Ala	Leu	Val	Trp	Val 440	Ile	Ala	Lys	Ser	Gly 445	Ile	Ser	Ser
25	Gln	Gln 450	Gln	Ser	Met	Arg	Leu 455	Ala	Asn	Leu	Leu	Met 460	Leu	Leu	Ser	His
ية .	Val 465	Arg	His	Ala	Ser	A sn 4 70	Lys	Gly	Met	Glu	His 475	Leu	Leu	Asn	Met	Lys 480
30	Cys	Lys	Asn	Val	Val 485	Pro	Val	Tyr	Asp	Leu 490	Leu	Leu	Glu	Met	Leu 495	Asn
25	Ala	His	Val	Leu 500	-	Gly	Cys	Lys	Ser 505		Ile	Thr	Gly	Ser 510	Glu	Cys
35	Ser	Pro	Ala 515		Asp	Ser	Lys	Ser 520	Lys	Glu	Gly	Ser	Gln 525	Asn	Pro	Gln

Ser Gln

	(2) INFORMATION FOR SEQ ID NO: 26:	
5	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 30 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2	26:
	GTGCGGATCC TCTCAAGACA TGGATATAAA	30
20	(2) INFORMATION FOR SEQ ID NO: 27:	
25	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 25 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: other nucleic acid	
30		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2	27:
35	AGTAACAGGG CTGGCGCAAC GGTTC	25
	(2) INFORMATION FOR SEQ ID NO: 28:	

(i) SEQUENCE CHARACTERISTICS:

(A)	LENGTH	:	22	bas	se	pair	c
(B)	TYPE:	nι	ıcle	eic	a	cid	
(C)	STRAND	ΕI	ONES	ss:	si	ingle	=

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ACTGGCGATG GACCACTAAA GG